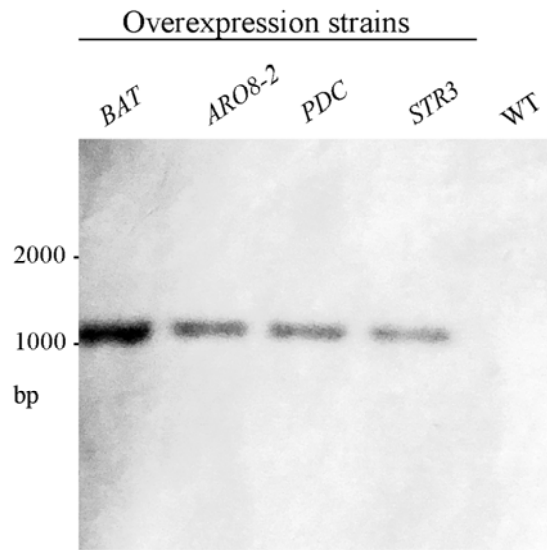


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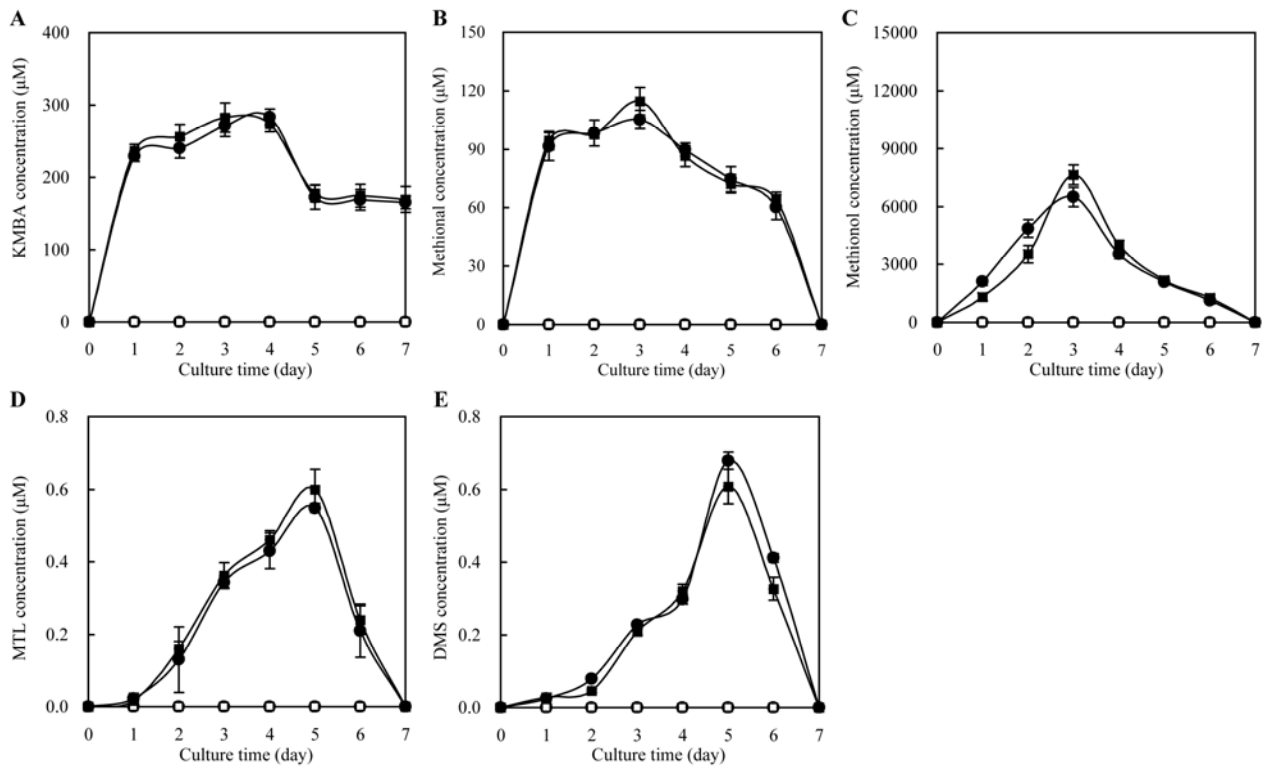
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6 **FIG S1** Southern blot analysis of gene overexpression in *C. rosea* using the *hpt* probe showing
7 hybridized signals in the overexpression strains. WT: wild type.

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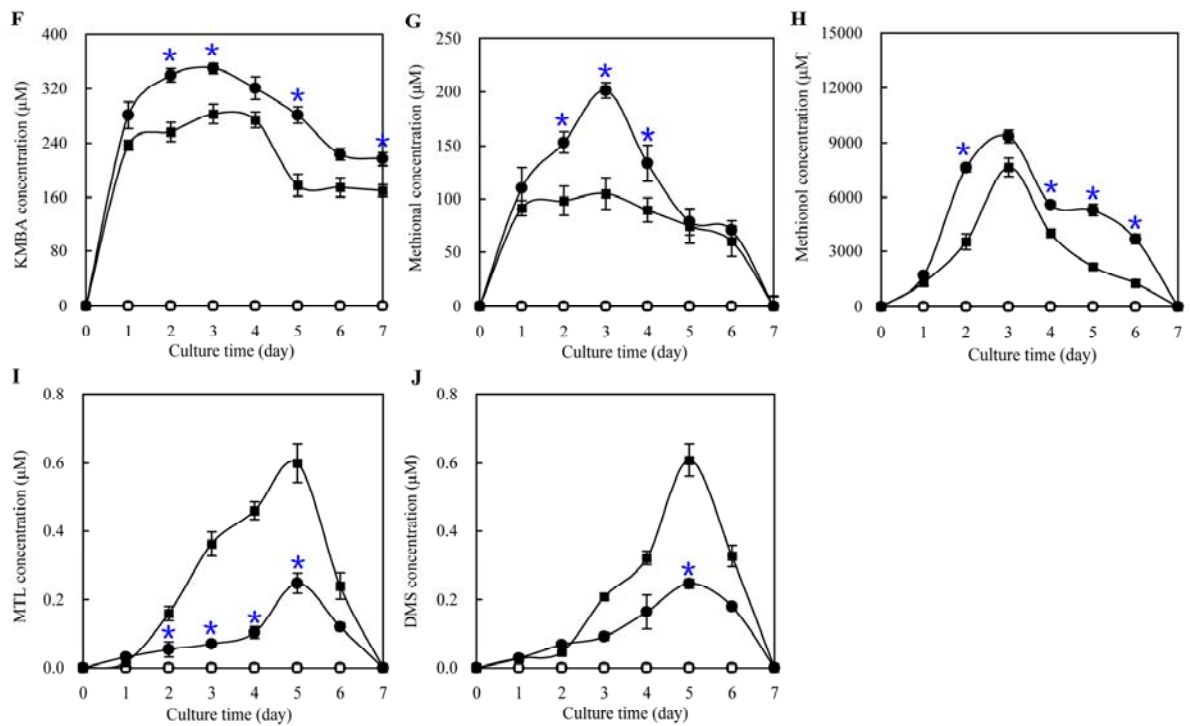
25 **Overexpressing *BAT* in *C. rosea***



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28 **Overexpressing *ARO8-2* in *C. rosea***



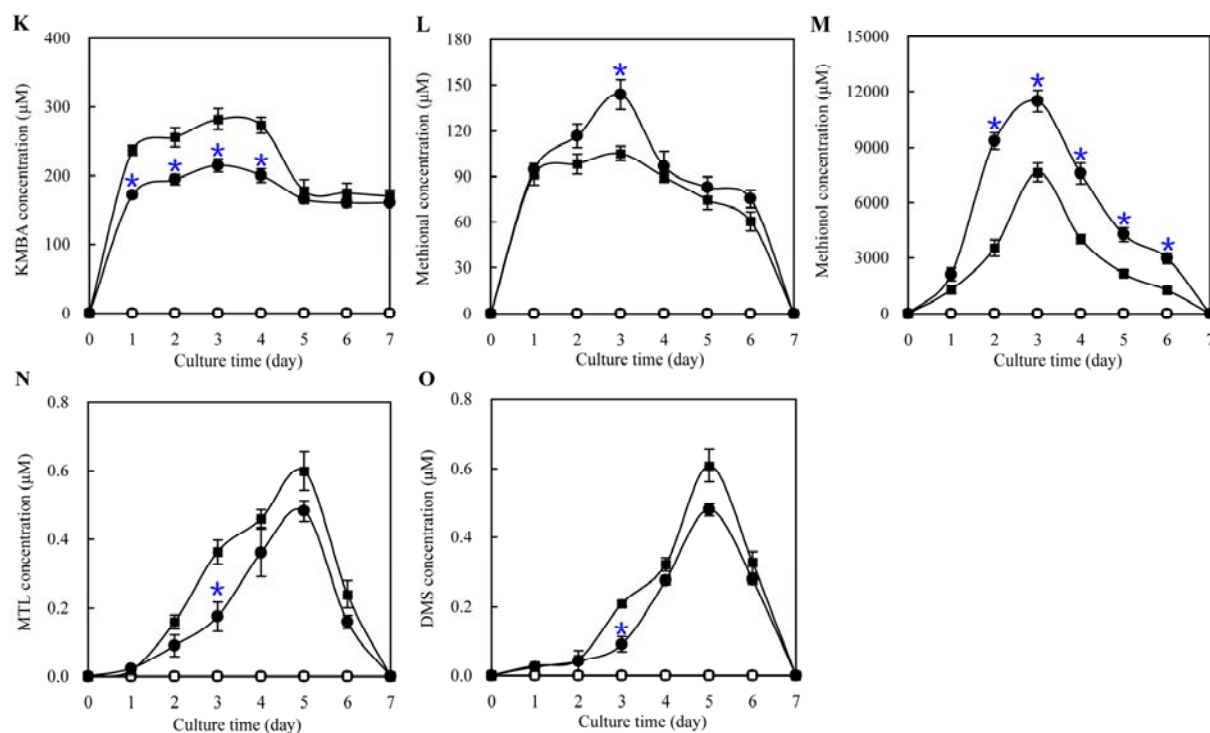
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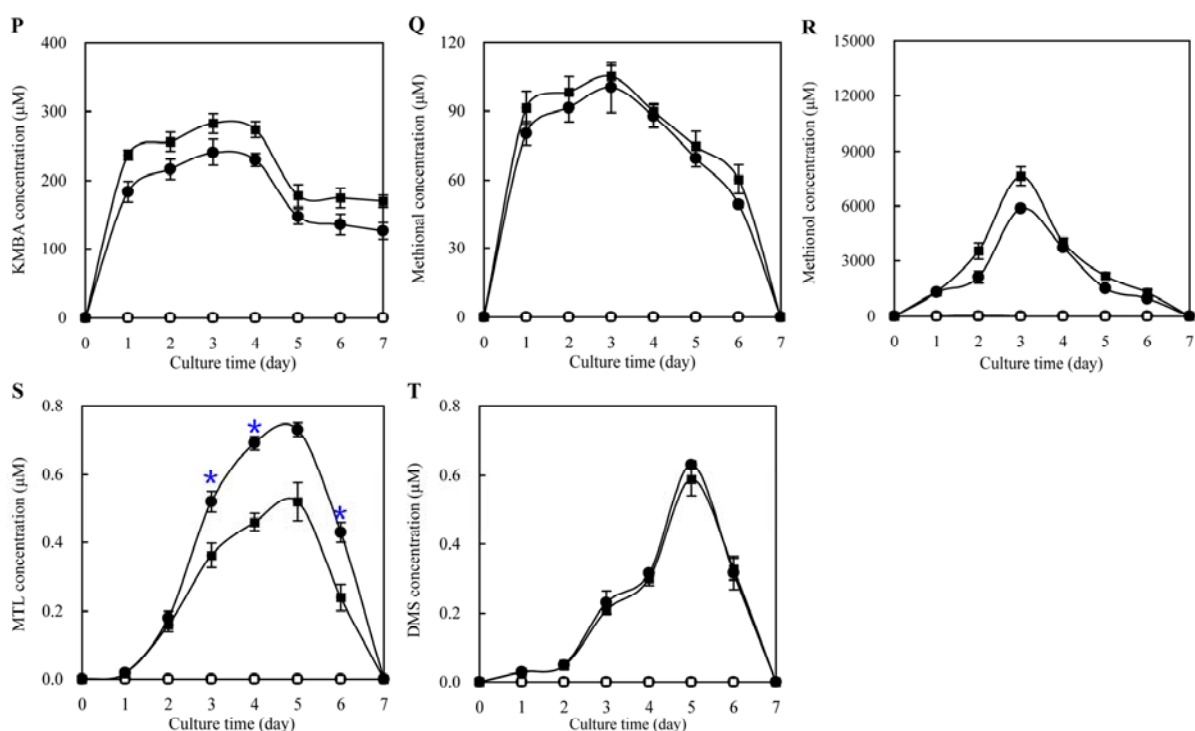
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33 **Overexpressing *PDC* in *C. rosea***



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35 **Overexpressing *STR3* in *C. rosea***



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37 **FIG S2** The catabolism of Met into VOSCs was influenced by the overexpression of *ARO8-2*, *PDC*
38 and *STR3*.

39 Wild-type strain cultured in growth media, \square ; wild-type strain was cultured in growth media added

40 with 5 g l⁻¹ Met, ■; overexpression strain cultured in growth media, ○; overexpression strain
41 cultured in growth medium added with 5 g l⁻¹ Met, ●. The experiments were performed in triplicate
42 with three independent repetitions and results are presented as mean values ± SD. Significant
43 difference between the wild type strain and overexpression strains treated with Met were measured
44 by using the *t*-test for independent samples. An asterisk indicates significant (P<0.05) difference
45 from the corresponding wild-type value. Statistical analyses were determined using SPSS software
46 package 19.0.

47 A-E. Overexpression of the aminotransferase gene *BAT* had no effect on VOSCs biosynthesis.

48 F-G. Overexpression of the aminotransferase gene *ARO8-2* stimulated the metabolism of the Ehrlich
49 pathway but suppressed the metabolism of the Demethiolation pathway.

50 K-O. Overexpression of the decarboxylase gene *PDC* decreased the production of KMBA,
51 stimulated the production of methional and methionol, and suppressed the metabolism of the
52 Demethiolation pathway.

53 P-T. Overexpression of the demethylase gene *STR3* decreased the production of KMBA and
54 methionol but increased the production of MTL.

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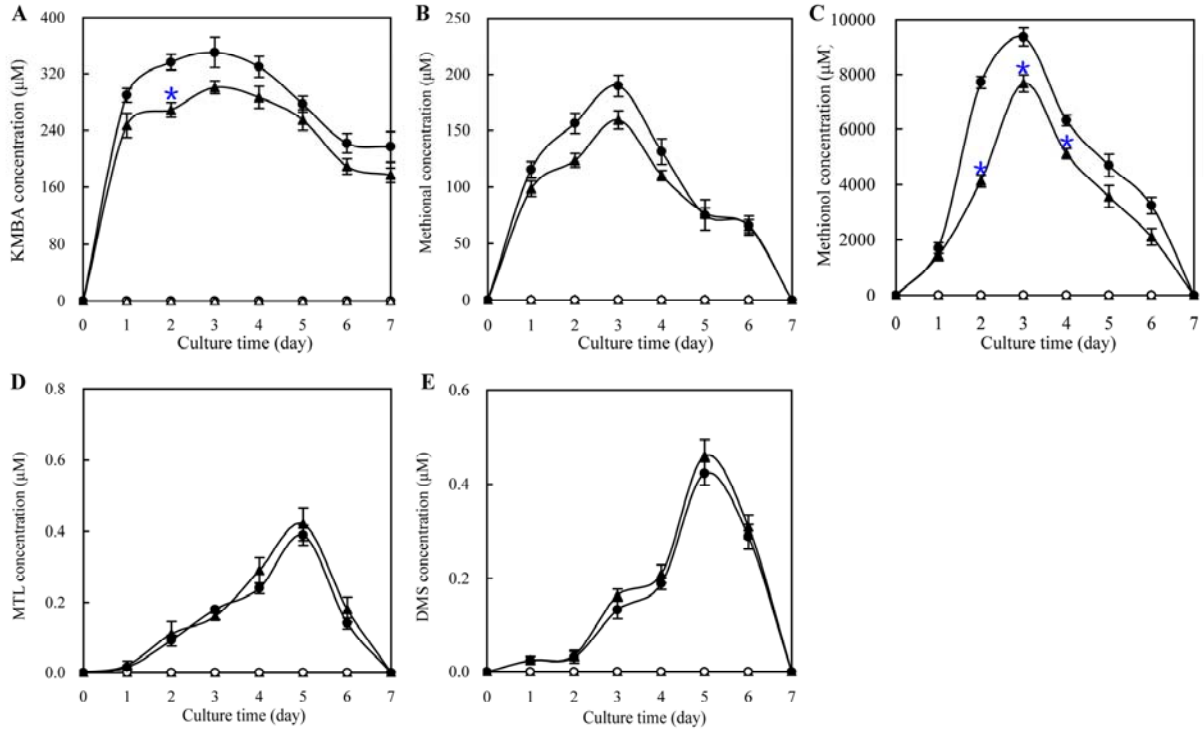
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67 **Overexpressing *ARO8-2* with deleted putative MSN2 binding site (-1160/-1156)**

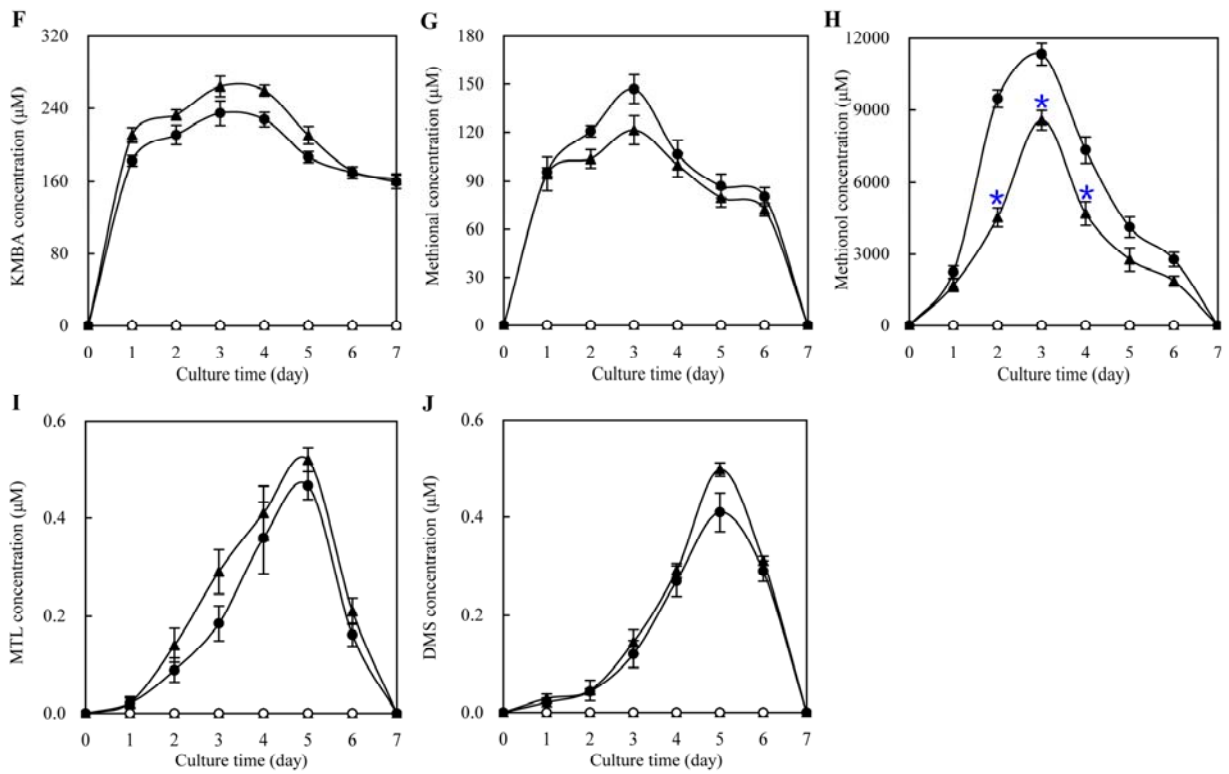


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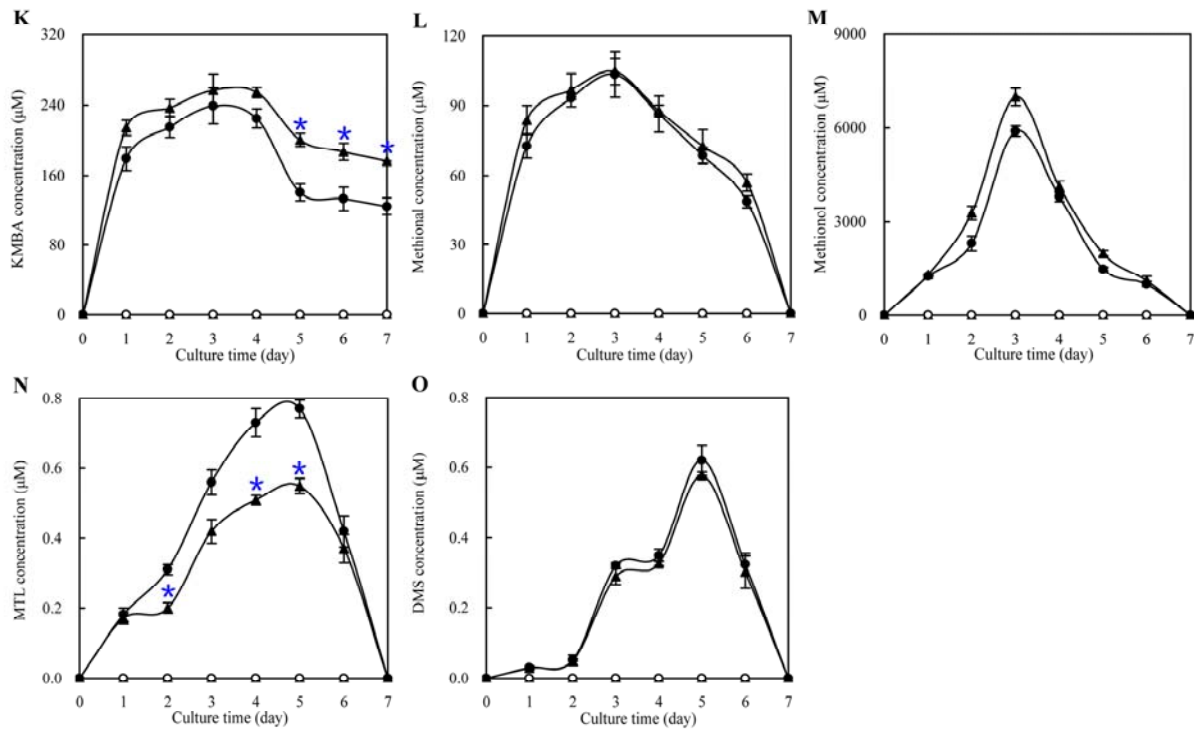
71 **Overexpressing *PDC* with deleted putative MSN2 binding site (-1255/-1251)**



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74 **Overexpressing *STR3* with deleted putative *GLN3* binding site (-512/-508)**



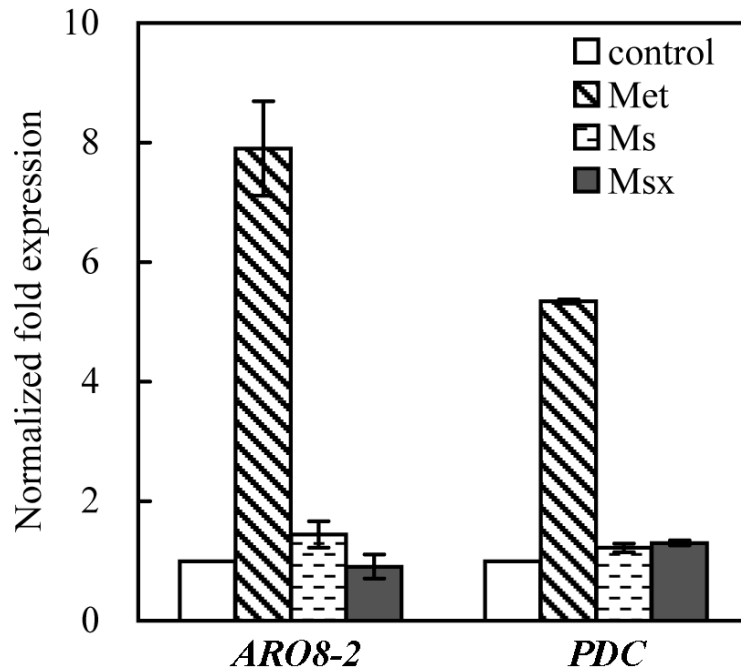
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76 **FIG S3** Essential binding motifs controlling the biosynthesis of VOCs from Met.

77 Putative *MSN2* binding site (-1160/-1156 of *ARO8-2* promoter) (A-E), *MSN2* binding site
78 (-1255/-1251 of *PDC* promoter) (F-J) and *GLN3* binding site (-512/-508, *STR3* promoter) (K-O)
79 were involved in the regulation of the catabolism of Met into VOCs. Overexpression strain
80 cultured in the growth media, ○; Overexpression strain cultured in the growth media added with 5 g
81 l⁻¹ Met, ●; Overexpression strain with TFBSs deleted cultured in the growth media, △;
82 Overexpression strain with TFBSs deleted cultured in the growth media added with 5 g l⁻¹ Met, ▲.
83 TFBSs: transcriptional factor binding sites. The experiments were performed in triplicate with three
84 independent repetitions and results are presented as mean values \pm SD. Significant difference
85 between the overexpression strains and TFBSs deletion strains treated with Met were measured by
86 using the *t*-test for independent samples. An asterisk indicates significant (P<0.05) difference from
87 the corresponding overexpression-type value. Statistical analyses were determined using SPSS
88 software package 19.0.

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97 **FIG S4** Met, but not Ms or Msx, stimulated the transcription of *ARO8-2* and *PDC*.

98 Ms: methionine sulfoxide, Msx: methionine sulfoximine.

99 The transcript of *ARO8-2* and *PDC* was detected using quantitative real-time PCR. Normalized fold
100 expression values for *ARO8-2* and *PDC* were calculated relative to the control inoculated into
101 growth media.

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